AMENDMENTS TO THE CLAIMS

Please cancel Claims 1-22 and enter Claims 23-44.

1-22. (Canceled)

23. (New) A method to identify a compound that inhibits the binding between an IgE antibody and a high-affinity FcεRIα protein, said method comprising:

(a) constructing a first three-dimensional model in which the protein backbone atoms have a root mean square deviation of less than 10 angstroms from the protein backbone atoms in a second three-dimensional model defined by atomic coordinates represented in Table 1; and

(b) using said first model of (a) to identify a compound that interacts with a site on either the human high affinity FcεRIα protein or the Fc-Cε3/Cε4 region of a human IgE protein, wherein such interaction indicates the compound is capable of inhibiting the binding between an IgE antibody and a high-affinity FcεRIα protein.

24. (New) The method of Claim 23, wherein said compound identification step comprises computational means to determine if a compound interacts with a site on either the human high affinity FcεRIα protein or the Fc-Cε3/Cε4 region of a human IgE protein.

25. (New) The method of Claim 23, wherein said compound identification step comprises:

(i) generating the spatial structure of a compound to be tested; and

(ii) using computer means to determine if said test compound interacts with a site on either the human high affinity FcεRIα protein or the Fc-Cε3/Cε4 region of a human IgE protein.

26. (New) The method of Claim 23, further comprising:

(c) obtaining the compound identified in step (b); and

(d) testing said compound obtained in step (c) in a FcεRIα protein/ IgE binding assay to determine if said compound inhibits the binding of the IgE antibody to the FcεRIα protein.

27. (New) The method of Claim 23, wherein said first three-dimensional model consists of protein backbone atoms having a root mean square deviation of less than 5 angstroms from the protein backbone atoms in said second three-dimensional model defined by atomic coordinates represented in Table 1.

28. (New) The method of Claim 23, wherein said first three-dimensional model is defined by atomic coordinates obtained by the steps of:

(a) producing a crystal of a complex between (i) a first protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:2 or SEQ ID NO:4, and (ii) a second protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:6, wherein said crystal belongs to spacegroup $P4_12_12$ or spacegroup R32; and

(b) performing x-ray diffraction analysis of the crystal produced in (a).

29. (New) The method of Claim 28, wherein said first protein consists of the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, and said second protein consists of the amino acid sequence of SEQ ID NO:6.

30. (New) The method of Claim 28, wherein said crystal is produced by the hanging drop method of vapor diffusion using a precipitant selected from the group consisting of:

(a) a precipitant comprising (i) about 100 mM Tris-(hydroxymethyl)aminomethane (TRIS) at a pH of about 8.5, (ii) ammonium sulfate in a range of from about 1.4 to about 1.6 mM and (iii) about 8 mM 3-[(3-Cholamidopropyl)Dimethyl-Ammonio]-1-Propanesulfonate (CHAPS) ; and

(b) a precipitant composed of (i) about 100 mM Tris-(hydroxymethyl)aminomethane (TRIS) at a pH of about 8.5 and (ii) ammonium sulfate in a range of from about 1.4 to about 1.6 mM.

31. (New) The method of Claim 28, wherein said first three-dimensional model is defined by the atomic coordinates represented in Table 1.

32. (New) A method to identify a compound that inhibits the binding between an IgE antibody and a high-affinity FcεRIα protein, said method comprising:

(a) constructing a first three-dimensional model in which the protein backbone atoms have a root mean square deviation of less than 10 angstroms from the backbone atoms in a second three-dimensional model defined by the atomic coordinates represented in Table 1; and,

(b) performing structure-based design to identify the structure of a compound predicted to interact with a site on the FcεRIa protein or the Fc-Cε3/Cε4 region of a human IgE protein, wherein such interaction indicates the compound is capable of inhibiting the binding between an IgE antibody and a high-affinity FcεRIα protein.

33. (New) The method of Claim 32, wherein said structure-based design step comprises (i) generating the spatial structure of the compound to be tested and (ii) using computer means and the compound structure to determine if the compound interacts with a site on the FcεRIa protein or the Fc-Cε3/Cε4 region of a human IgE protein, wherein such interaction indicates the compound is capable of inhibiting the binding between an IgE antibody and a high-affinity FcεRIα protein.

34. (New) The method of Claim 32, further comprising:

(c) synthesizing said compound identified in step (b); and,

(d) testing said synthesized compound in a FcεRIα protein/ IgE binding assay to determine if said compound inhibits the binding of the IgE antibody to the FcεRIα protein.

35. (New) The method of Claim 32, wherein said first three-dimensional model is defined by the atomic coordinates represented in Table 1.

36. (New) The method of Claim 32, wherein said first three-dimensional model is defined by atomic coordinates obtained by the steps of:

(a) producing a crystal of a complex between (i) a first protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:2 or SEQ ID NO:4, and (ii) a second protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:6, wherein said crystal belongs to spacegroup $P4_12_12$ or spacegroup R32; and

(b) performing x-ray diffraction analysis of the crystal produced in (a).

37. (New) The method of Claim 32, wherein said first protein consists of the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, and said second protein consists of the amino acid sequence of SEQ ID NO:6.

38. (New) The method of Claim 32, wherein said crystal is produced by the hanging drop method of vapor diffusion using a precipitant selected from the group consisting of:

(a) a precipitant comprising (i) about 100 mM Tris-(hydroxymethyl)aminomethane (TRIS) at a pH of about 8.5, (ii) ammonium sulfate in a range of about 1.4 to about 1.6 mM and (iii) about 8 mM 3-[(3-Cholamidopropyl)Dimethyl-Ammonio]-1-Propanesulfonate (CHAPS) ; and

(b) a precipitant composed of (i) about 100 mM Tris-(hydroxymethyl)aminomethane (TRIS) at a pH of about 8.5 and (ii) ammonium sulfate in a range of about 1.4 to about 1.6 mM.

39. (New) A method to identify a compound that inhibits the binding between an IgE antibody and a high-affinity FcεRIα protein, said method comprising:

(a) constructing a three-dimensional model in which the protein backbone atoms have a root mean square deviation of less than 10 angstroms from the backbone atoms in a three-dimensional model defined by atomic coordinates represented in Table 1; and,

(b) using computing means to screen a compound structure obtained from a database to identify the structure of a compound predicted to interact with a site on the FcεRIa protein or the

Fc-Cε3/Cε4 region of a human IgE protein, wherein such interaction indicates the compound is capable of inhibiting the binding between an IgE antibody and a high-affinity FcεRIα protein.

40. (New) The method of Claim 39, wherein said structure-based design step comprises (i) generating the spatial structure of the compound to be tested and (ii) using computer means and the compound structure to determine if the compound interacts with a site on the FcεRIa protein or the Fc-Cε3/Cε4 region of a human IgE protein, wherein such interaction indicates the compound is capable of inhibiting the binding between an IgE antibody and a high-affinity FcεRIα protein.

41. (New) The method of Claim 39, further comprising:

(c) synthesizing said compound identified in step (b); and,

(d) testing said synthesized compound in a FcεRIα protein/ IgE binding assay to determine if said compound inhibits the binding of the IgE antibody to the FcεRIα protein.

42. (New) The method of Claim 39, wherein said first three-dimensional model is defined by atomic coordinates obtained by the steps of:

(a) producing a crystal of a complex between (i) a first protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:2 or SEQ ID NO:4, and (ii) a second protein consisting of an amino acid sequence at least about 95% identical to SEQ ID NO:6, wherein said crystal belongs to spacegroup $P4_12_12$ or spacegroup R32; and

(b) performing x-ray diffraction analysis of the crystal produced in (a).

43. (New) The method of Claim 39, wherein said first protein consists of the amino acid sequence of SEQ ID NO:2 or SEQ ID NO:4, and said second protein consists of the amino acid sequence of SEQ ID NO:6.

44. (New) The method of Claim 39, wherein said first three-dimensional model is defined by the atomic coordinates represented in Table 1.